

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Choi, Yongwon
Wong, Brian
Josien, Regis
Steinman, Ralph

(ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-200 CIP

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1823 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

1001910 11401

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT	48
Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr	
1 5 10 15	
AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG	96
Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu	
20 25 30	
GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA	144
Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys	
35 40 45	
CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA	192
Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly	
50 55 60	
TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA	240
Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu	
65 70 75 80	
GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC	288
Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu	
85 90 95	
ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG	336
Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu	
100 105 110	
TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT	384
Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr	
115 120 125	
TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG	432
Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu	
130 135 140	
TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT	480
Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala	
145 150 155 160	

100194012401

ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA	528
Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys	
165 170 175	
ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG	576
Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp	
180 185 190	
TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT	624
Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe	
195 200 205	
TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC	672
Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro	
210 215 220	
TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA	720
Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys	
225 230 235 240	
GTT CGA GAT ATA GAT TGA GCGCCAGTTT TTGGAGTGTT ATGTATTTCC	768
Val Arg Asp Ile Asp *	
245	
TGGATGTTTG GAAACATTTT TTAAACAAG CCAAGAAAGA TGTATATAGG TGTGTGAGAC	828
TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA CCTTGTAGAG	888
AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC ACAATGGTTT	948
TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTTGACCTT	1008
ATGAGAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTCATGTGC CCCTTCGCAG	1068
CTGAAGTGGA GAGGGTGTCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG GCAAATTCCTT	1128
TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA GGAGAGAAAA	1188
TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTTCAGA TGTAATGTTT TCTTTGCAAA	1248
GTATTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA ATATTTAAAA ATGTCTTGCT	1308
GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT TTGTAAATTC	1368
CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCCTAATA TCAAATGCAG	1428
TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTCAG ACTTGTCAG CCTGTGCAAA	1488
AAAATTAAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT GCCTTTCAAA	1548
TTTAGAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC	1608
TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTTCCAC AAGTGCCGCA	1668

AATTGTACCT TTTTGTGTTT TTTTCAAAAT AGAAAAGTTA TTAGTGTTT ATCAGCAAAA 1728
AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAAC ATTGCCTTG 1788
AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC 1823

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	1	5	10	15
Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	Ala	Asp	Phe	Gln	Asp	Thr	Thr	Leu	20	25	30	
Glu	Ser	Gln	Asp	Thr	Lys	Leu	Ile	Pro	Asp	Ser	Cys	Arg	Arg	Ile	Lys	35	40	45	
Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys	Glu	Leu	Gln	His	Ile	Val	Gly	50	55	60	
Ser	Gln	His	Ile	Arg	Ala	Glu	Lys	Ala	Met	Val	Asp	Gly	Ser	Trp	Leu	65	70	75	80
Asp	Leu	Ala	Lys	Arg	Ser	Lys	Leu	Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	85	90	95	
Thr	Ile	Asn	Ala	Thr	Asp	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Ser	Leu	100	105	110	
Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Gly	Lys	Ile	Ser	Asn	Met	Thr	115	120	125	
Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val	Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	130	135	140	
Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	145	150	155	160
Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val	Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	165	170	175	
Ile	Pro	Ser	Ser	His	Thr	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	180	185	190	

10019101404

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
 195 200 205

Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
 210 215 220

Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
 225 230 235 240

Val Arg Asp Ile Asp *
 245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 142..1092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCACGTCCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCGGGGCG GGGGCCGTGG	60
CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC	120
CCGAACTCCG GGCGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG	171
Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys	
250 255	
TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC	219
Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His	
260 265 270	
GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA	267
Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro	
275 280 285	
CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG	315
Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu	
290 295 300	

1001910 12101

GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG	363
Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln	
305 310 315 320	
ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA	411
Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg	
325 330 335	
ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG	459
Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu	
340 345 350	
AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT	507
Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe	
355 360 365	
CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC	555
Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg	
370 375 380	
TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC	603
Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala	
385 390 395 400	
CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT	651
Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn	
405 410 415	
GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG	699
Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp	
420 425 430	
TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC	747
Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn	
435 440 445	
GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC	795
Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn	
450 455 460	
ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT	843
Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr	
465 470 475 480	
CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT	891
Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser	
485 490 495	
TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT	939
Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn	
500 505 510	
TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC	987
Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu	

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515	520	525	
CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG			1035
Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu			
530	535	540	
GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC			1083
Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp			
545	550	555	560
ATA GAC TGA GACTCATTTC GTGGAACATT AGCATGGATG TCCTAGATGT			1132
Ile Asp *			
TTGGAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG			1192
GCCACGGTG TATGAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT TGTGTATATG			1252
TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTTAC AATTTTGTA			1312
TGATTTCTTA GAATGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA AAAACTTACA			1372
CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA			1432
ACCTTGAAAT TAAGAGGATG CCATGTCATT GCATAGAAAT GATAGTGTGA AGGGTTAAGT			1492
TCTTTTGAAT TGTTACATTG CGCTGGGACC TGCAAATAAG TTCTTTTTTT CTAATGAGGA			1552
GAAAAATATA TGTATTTTTA TATAATGTCT AAAGTTATAT TTCAGGTGTA ATGTTTTCTG			1612
TGCAAAGTTT TGTAATTAT ATTTGTGCTA TAGTATTTGA TTCAAATAT TTAATAATGT			1672
CTCACTGTTG ACATATTTAA TGTTTTAAAT GTACAGATGT ATTTAACTGG TGCACTTTGT			1732
AATCCCCCTG AAGGTACTCG TAGCTAAGGG GGCAGAATAC TGTTTCTGGT GACCACATGT			1792
AGTTTATTTT TTTATTCTTT TTAAGTTAAT AGAGTCTTCA GACTTGTCAC AACTATGCAA			1852
GCAAAATAAA TAAATAAAAA TAAATGAAT ACCTTGAATA ATAAGTAGGA TGTGGTCAC			1912
CAGGTGCCTT TCAAATTTAG AAGCTAATTG ACTTTAGGAG CTGACATAGC CAAAAGGAA			1972
CATAATAGGC TACTGAAATC TGTCAGGAGT ATTTATGCAA TTATTGAACA GGTGTCTTTT			2032
TTTACAAGAG CTACAAATTG TAAATTTTGG TTTCTTTTTT TTCCCATAGA AAATGTACTA			2092
TAGTTTATCA GCCAAAAAAC AATCCACTTT TTAATTTAGT GAAAGTTATT TTATTATACT			2152
GTACAATAAA AGCATTGTCT CTGAATGTTA ATTTTTTGGT ACAAAAAATA AATTGTACG			2212
AAAAAAAAAA AAAAAAAAAA AAAAA			2237

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
1 5 10 15

Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
20 25 30

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225 230 235 240

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Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
260 265 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
275 280 285

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
290 295 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp *
305 310 315

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gln Gln Pro Met Asn Tyr Pro Cys Pro Gln Ile Phe Trp Val Asp
1 5 10 15

Ser Ser Ala Thr Ser Ser Trp Ala Pro Pro Gly Ser Val Phe Pro Cys
20 25 30

Pro Ser Cys Gly Pro Arg Gly Pro Asp Gln Arg Arg Pro Pro Pro Pro
35 40 45

Pro Pro Pro Val Ser Pro Leu Pro Pro Pro Ser Gln Pro Leu Pro Leu
50 55 60

Pro Pro Leu Thr Pro Leu Lys Lys Lys Asp His Asn Thr Asn Leu Trp
65 70 75 80

Leu Pro Val Val Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly
85 90 95

Leu Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu

10047910 121401

100	105	110
Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln 115 120 125		
Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val 130 135 140		
Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp 145 150 155 160		
Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys 165 170 175		
Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys 180 185 190		
Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys 195 200 205		
Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu 210 215 220		
Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser 225 230 235 240		
Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr 245 250 255		
Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr 260 265 270		
Phe Phe Gly Leu Tyr Lys Leu 275		

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Mus musculus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Pro Ser Ser Gly Ala Leu Lys Asp Leu Ser Phe Ser Gln His Phe
 1 5 10 15
 Arg Met Met Val Ile Cys Ile Val Leu Leu Gln Val Leu Leu Gln Ala
 20 25 30
 Val Ser Val Ala Val Thr Tyr Met Tyr Phe Thr Asn Glu Met Lys Gln
 35 40 45
 Leu Gln Asp Asn Tyr Ser Lys Ile Gly Leu Ala Cys Phe Ser Lys Thr
 50 55 60
 Asp Glu Asp Phe Trp Asp Ser Thr Asp Gly Glu Ile Leu Asn Arg Pro
 65 70 75 80
 Cys Leu Gln Val Lys Arg Gln Leu Tyr Gln Leu Ile Glu Glu Val Thr
 85 90 95
 Leu Arg Thr Phe Gln Asp Thr Ile Ser Thr Val Pro Glu Lys Gln Leu
 100 105 110
 Ser Thr Pro Pro Leu Pro Arg Gly Gly Arg Pro Gln Lys Val Ala Ala
 115 120 125
 His Ile Thr Gly Ile Thr Arg Arg Ser Asn Ser Ala Leu Ile Pro Ile
 130 135 140
 Ser Lys Asp Gly Lys Thr Leu Gly Gln Lys Ile Glu Ser Trp Glu Ser
 145 150 155 160
 Ser Arg Lys Gly His Ser Phe Leu Asn His Val Leu Phe Arg Asn Gly
 165 170 175
 Glu Leu Val Ile Glu Gln Glu Gly Leu Tyr Tyr Ile Tyr Ser Gln Thr
 180 185 190
 Tyr Phe Arg Phe Gln Glu Ala Glu Asp Ala Ser Lys Met Val Ser Lys
 195 200 205
 Asp Lys Val Arg Thr Lys Gln Leu Val Gln Tyr Ile Tyr Lys Tyr Thr
 210 215 220
 Ser Tyr Pro Asp Pro Ile Val Leu Met Lys Ser Ala Arg Asn Ser Cys
 225 230 235 240
 Trp Ser Arg Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly
 245 250 255
 Leu Phe Glu Leu Lys Lys Asn Asp Arg Ile Phe Val Ser Val Thr Asn
 260 265 270
 Glu His Leu Met Asp Leu Asp Gln Glu Ala Ser Phe Phe Gly Ala Phe
 275 280 285

1004910 1440

Leu Ile Asn
290

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Thr Arg Gly Leu Gln Gly Leu Gly Gly Arg Pro Gln Gly Arg
1 5 10 15
Gly Cys Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu
20 25 30
Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
35 40 45
Gln Asp Gln Gly Arg Arg Val Glu Lys Ile Ile Gly Ser Gly Ala Gln
50 55 60
Ala Gln Lys Arg Leu Asp Asp Ser Lys Pro Ser Cys Ile Leu Pro Ser
65 70 75 80
Pro Ser Ser Leu Ser Glu Thr Pro Asp Pro Arg Leu His Pro Gln Arg
85 90 95
Ser Asn Ala Ser Arg Asn Leu Ala Ser Thr Ser Gln Gly Pro Val Ala
100 105 110
Gln Ser Ser Arg Glu Ala Ser Ala Trp Met Thr Ile Leu Ser Pro Ala
115 120 125
Ala Asp Ser Thr Pro Asp Pro Gly Val Gln Gln Leu Pro Lys Gly Glu
130 135 140
Pro Glu Thr Asp Leu Asn Pro Glu Leu Pro Ala Ala His Leu Ile Gly
145 150 155 160
Ala Trp Met Ser Gly Gln Gly Leu Ser Trp Glu Ala Ser Gln Glu Glu
165 170 175

10019910-12401

Ala Phe Leu Arg Ser Gly Ala Gln Phe Ser Pro Thr His Gly Leu Ala
180 185 190

Leu Pro Gln Asp Gly Val Tyr Tyr Leu Tyr Cys His Val Gly Tyr Arg
195 200 205

Gly Arg Thr Pro Pro Ala Gly Arg Ser Arg Ala Arg Ser Leu Thr Leu
210 215 220

Arg Ser Ala Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Arg Gly Ser Pro
225 230 235 240

Glu Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Val Asp Pro
245 250 255

Ile Gly Tyr Gly Ser Leu Trp Tyr Thr Ser Val Gly Phe Gly Gly Leu
260 265 270

Ala Gln Leu Arg Ser Gly Glu Arg Val Tyr Val Asn Ile Ser His Pro
275 280 285

Asp Met Val Asp Tyr Arg Arg Gly Lys Thr Phe Phe Gly Ala Val Met
290 295 300

Val Gly
305

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1 5 10 15

Leu Pro Gln Lys Met Gly Gly Phe Gln Asn Ser Arg Arg Cys Leu Cys
20 25 30

Leu Ser Leu Phe Ser Phe Leu Leu Val Ala Gly Ala Thr Thr Leu Phe

10019101401

[illegible]

ATGAAGATCC TGACCGAGCG

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACTTGCGCT GAGGAGGAGC

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCTGAGACTC CATGAAAACG C

21

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAACCCTTAG TTTCCGTTG C

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCCAGATGG ACTTCTGTGG

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTCCTTCGA CGTGCTAACG

20

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